Figure 1. Monte Carlo population coverage analysis for HBV candidate epitopes

Frequency of genotypes

0.0000 0.0500 0.1000 0.1500 0.2000

No. epitopes recognized

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28

average no. epitopes recognized: 12.4

0 10 20 30 40 50 60 70 80 90 100

% population coverage
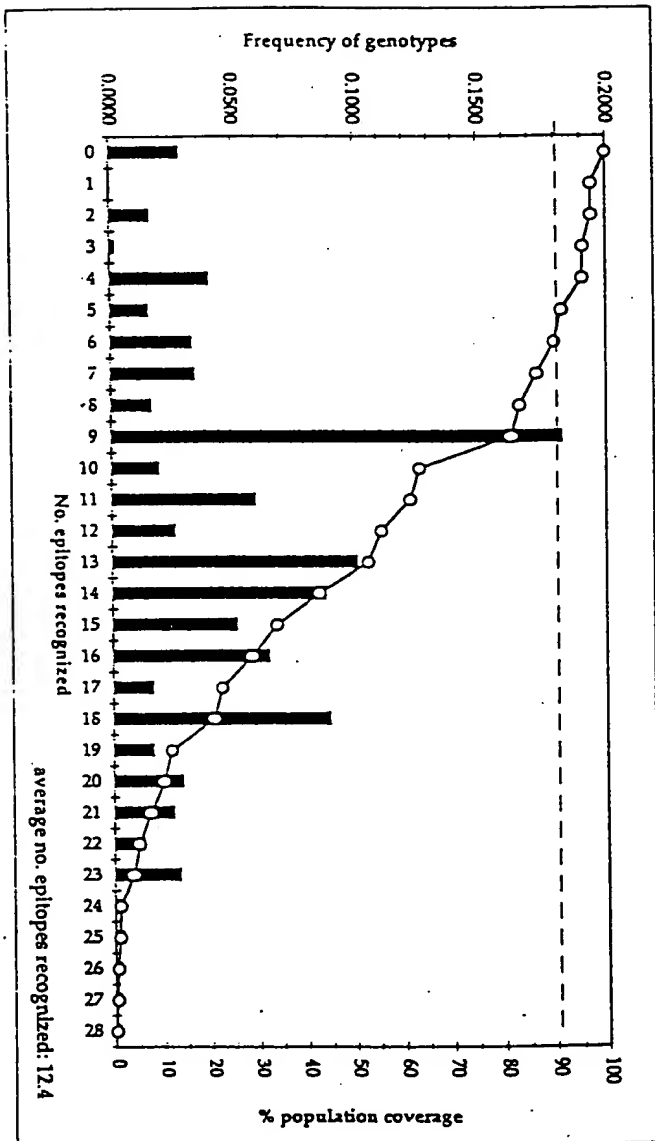
Monte Carlo population coverage analysis for HBV candidate epitopes

Plot of total frequency of genotypes as a function of the number of HBV candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each Hil population cluster in proportion to the relative frequency of the cluster within the HLA specified population.
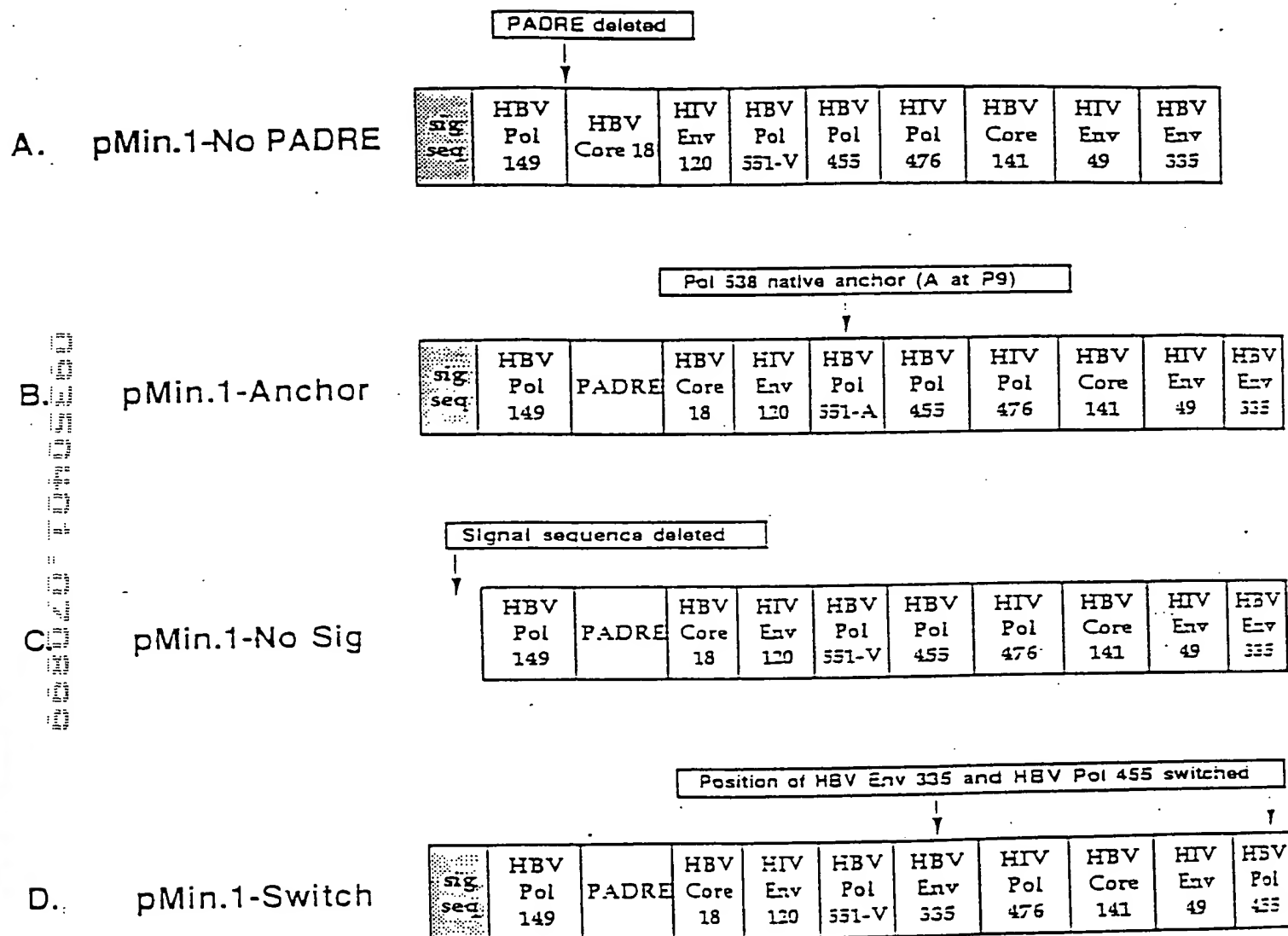
A. pMin.1-No PADRE

PADRE deleted

sig seq	HBV Pol 149	HBV Core 18	HIV Env 120	HBV Pol 551-V	HBV Pol 455	HIV Pol 476	HBV Core 141	HIV Env 49	HBV Env 335

B. pMin.1-Anchor

Pol 538 native anchor (A at P9)

sig seq	HBV Pol 149	PADRE	HBV Core 18	HIV Env 120	HBV Pol 551-A	HBV Pol 455	HIV Pol 476	HBV Core 141	HIV Env 49	HBV Env 335

C. pMin.1-No Sig

Signal sequence deleted

HBV Pol 149	PADRE	HBV Core 18	HIV Env 120	HBV Pol 551-V	HBV Pol 455	HIV Pol 476	HBV Core 141	HIV Env 49	HBV Env 335

D. pMin.1-Switch

Position of HBV Env 335 and HBV Pol 455 switched

sig seq	HBV Pol 149	PADRE	HBV Core 18	HIV Env 120	HBV Pol 551-V	HBV Env 335	HIV Pol 476	HBV Core 141	HIV Env 49	HBV Pol 455

FIGURE 2